
Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=9; day=3; hr=15; min=5; sec=1; ms=718;]

Validated By CRFValidator v 1.0.3

Application No: 10511130 Version No: 3.0

Input Set:

Output Set:

Started: 2009-09-02 16:37:05.223

Finished: 2009-09-02 16:37:08.641

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 418 ms

Total Warnings: 23

Total Errors: 0

No. of SeqIDs Defined: 33

Actual SeqID Count: 33

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W	213	Artificial or Unknown found in <213> in SEQ ID (3)
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W	213	Artificial or Unknown found in <213> in SEQ ID (9)
W	213	Artificial or Unknown found in <213> in SEQ ID (10)
W	213	Artificial or Unknown found in <213> in SEQ ID (11)
W	402	Undefined organism found in <213> in SEQ ID (12)
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W	402	Undefined organism found in <213> in SEQ ID (19)
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Input Set:

Output Set:

Started: 2009-09-02 16:37:05.223

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Total Warnings: 23
Total Errors: 0

No. of SeqIDs Defined: 33

Actual SeqID Count: 33

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Arg Thr Phe	Arg Pro	Tyr Ile	Tyr A	Ala Leu	Leu Arg	Asp 45	Asp Sei	Lys
Ile Glu Glu 50	Val Lys	Lys Ile 55	Thr G	Gly Glu	Arg His 60	Gly	Lys Il∈	e Val
Arg Ile Val	Asp Val	Glu Lys 70	Val G	Glu Lys	Lys Phe 75	Leu	Gly Ly:	Pro 80
Ile Thr Val	Trp Lys 85	Leu Tyr	Leu G	Glu His 90	Pro Gln	Asp	Val Pro	o Thr
Ile Arg Glu	Lys Val	Arg Glu		Pro Ala	Val Val	-	Ile Phe	e Glu
Tyr Asp Ile 115	Pro Phe	Ala Lys	Arg T	ſyr Leu	Ile Asp	Lys 125	Gly Leı	ı Ile
Pro Met Glu 130	Gly Glu	Glu Glu 135	Leu I	Lys Ile	Leu Ala 140	Phe	Asp Ile	e Glu
Thr Leu Tyr 145	His Glu	Gly Glu 150	Glu P	Phe Gly	Lys Gly 155	Pro	Ile Ile	Met 160
Ile Ser Tyr	Ala Asp 165	Glu Asn	Glu A	Ala Lys 170	Val Ile	Thr	Trp Lys	
Ile Asp Leu	Pro Tyr 180	Val Glu		/al Ser 185	Ser Glu	_	Glu Met 190	: Ile
Lys Arg Phe 195	Leu Arg	Ile Ile	Arg 6	Glu Lys	Asp Pro	Asp 205	Ile Ile	e Val
Thr Tyr Asn 210	Gly Asp	Ser Phe 215	Asp P	Phe Pro	Tyr Leu 220	Ala	Lys Arç	g Ala
Glu Lys Leu 225	Gly Ile	Lys Leu 230	Thr I	[le Gly	Arg Asp 235	Gly	Ser Glı	240

Lys Me	t Gln	Arg	Ile 245	Gly	Asp	Met	Thr	Ala 250	Val	Glu	Val	Lys	Gly 255	Arg
Ile Hi	s Phe	Asp 260	Leu	Tyr	His	Val	Ile 265	Thr	Arg	Thr	Ile	Asn 270	Leu	Pro
Thr Ty	r Thr 275	Leu	Glu	Ala	Val	Tyr 280	Glu	Ala	Ile	Phe	Gly 285	Lys	Pro	Lys
Glu Ly 29		Tyr	Ala	Asp	Glu 295	Ile	Ala	Lys	Ala	Trp 300	Glu	Ser	Gly	Glu
Asn Le 305	u Glu	Arg	Val	Ala 310	Lys	Tyr	Ser	Met	Glu 315	Asp	Ala	Lys	Ala	Thr 320
Tyr Gl	u Leu	Gly	Lys 325	Glu	Phe	Leu	Pro	Met 330	Glu	Ile	Gln	Leu	Ser 335	Arg
Leu Va	l Gly	Gln 340	Pro	Leu	Trp	Asp	Val 345	Ser	Arg	Ser	Ser	Thr 350	Gly	Asn
Leu Va	1 Glu 355	Trp	Phe	Leu	Leu	Arg 360	Lys	Ala	Tyr	Glu	Arg 365	Asn	Glu	Val
Ala Pr 37		Lys	Pro	Ser	Glu 375	Glu	Glu	Tyr	Gln	Arg 380	Arg	Leu	Arg	Glu
Ser Ty 385	r Thr	Gly	Gly	Phe 390	Val	Lys	Glu	Pro	Glu 395	Lys	Gly	Leu	Trp	Glu 400
Asn Il	e Val	Tyr	Leu 405	Asp	Phe	Arg	Ala	Leu 410	Tyr	Pro	Ser	Ile	Ile 415	Ile
Thr Hi	s Asn	Val 420	Ser	Pro	Asp	Thr	Leu 425	Asn	Leu	Glu	Gly	Cys 430	Lys	Asn
Tyr As	p Ile 435	Ala	Pro	Gln	Val	Gly 440	His	Lys	Phe	Cys	Lys 445	Asp	Ile	Pro
Gly Ph 45		Pro	Ser	Leu	Leu 455	Gly	His	Leu	Leu	Glu 460	Glu	Arg	Gln	Lys

Ile 465	Lys	Thr	Lys	Met	Lys 470	Glu	Thr	Gln	Asp	Pro 475	Ile	Glu	Lys	Ile	Leu 480
Leu	Asp	Tyr	Arg	Gln 485	Lys	Ala	Ile	Lys	Leu 490	Leu	Ala	Asn	Ser	Phe 495	Tyr
Gly	Tyr	Tyr	Gly 500	Tyr	Ala	Lys	Ala	Arg 505	Trp	Tyr	Cys	Lys	Glu 510	Cys	Ala
Glu	Ser	Val 515	Thr	Ala	Trp	Gly	Arg 520	Lys	Tyr	Ile	Glu	Leu 525	Val	Trp	Lys
Glu	Leu 530	Glu	Glu	Lys	Phe	Gly 535	Phe	Lys	Val	Leu	Tyr 540	Ile	Asp	Thr	Asp
Gly 545	Leu	Tyr	Ala	Thr	Ile 550	Pro	Gly	Gly	Glu	Ser 555	Glu	Glu	Ile	Lys	Lys 560
Lys	Ala	Leu	Glu	Phe 565	Val	Lys	Tyr	Ile	Asn 570	Ser	Lys	Leu	Pro	Gly 575	Leu
Leu	Glu	Leu	Glu 580	Tyr	Glu	Gly	Phe	Tyr 585	Lys	Arg	Gly	Phe	Phe 590	Val	Thr
Lys	Lys	Arg 595	Tyr	Ala	Val	Ile	Asp 600	Glu	Glu	Gly	Lys	Val 605	Ile	Thr	Arg
Gly	Leu 610	Glu	Ile	Val	Arg	Arg 615	Asp	Trp	Ser	Glu	Ile 620	Ala	Lys	Glu	Thr
Gln 625	Ala	Arg	Val	Leu	Glu 630	Thr	Ile	Leu	Lys	His 635	Gly	Asp	Val	Glu	Glu 640
Ala	Val	Arg	Ile	Val 645	Lys	Glu	Val	Ile	Gln 650	Lys	Leu	Ala	Asn	Tyr 655	Glu
Ile	Pro	Pro	Glu 660	Lys	Leu	Ala	Ile	Tyr 665	Glu	Gln	Ile	Thr	Arg 670	Pro	Leu
His	Glu	Tyr 675	Lys	Ala	Ile	Gly	Pro 680	His	Val	Ala	Val	Ala 685	Lys	Lys	Leu

Ala Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile

690 695 700

Val Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu 705 710 715 720

Glu Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu
725 730 735

Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr \$740\$ \$750\$

Arg Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr 755 760 765

Ser Trp Leu Asn Ile Lys Lys Ser 770 775

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<212> PRT

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Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile 35 40 45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg $50 \hspace{1.5cm} 55 \hspace{1.5cm} 60 \hspace{1.5cm}$

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile 65 70 75 80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile 85 90 95

Arg Glu Lys	Val Arg 100	Glu His		la Val v	Val Asp	Ile Phe		Tyr
Asp Ile Pro	Phe Ala	Lys Arg	Tyr Le	eu Ile <i>i</i>	Asp Lys	Gly Leu 125	ılle	Pro
Met Glu Gly 130	Glu Glu	Glu Leu 135	Lys Il	le Leu <i>i</i>	Ala Phe 140	Asp Ile	Glu	Thr
Leu Tyr His 145	Glu Gly	Glu Glu 150	Phe Gl		Gly Pro 155	Ile Ile	Met	Ile 160
Ser Tyr Ala	Asp Glu 165	Asn Glu	Ala Ly	ys Val : 170	Ile Thr	Trp Lys	175	Ile
Asp Leu Pro	Tyr Val	Glu Val	Val Se		Glu Arg	Glu Met		Lys
Arg Phe Leu 195	Arg Ile	Ile Arg	Glu L <u>y</u> 200	ys Asp I	Pro Asp	Ile Ile 205	· Val	Thr
Tyr Asn Gly 210	Asp Ser	Phe Asp 215	Phe Pi	ro Tyr 1	Leu Ala 220	Lys Arc	Ala	Glu
Lys Leu Gly 225	Ile Lys	Leu Thr 230	Ile Gl		Asp Gly 235	Ser Glu	Pro	Lys 240
Met Gln Arg	Ile Gly 245	Asp Met	Thr Al	la Val (250	Glu Val	Lys Gly	Arg 255	Ile
His Phe Asp	Leu Tyr 260	His Val	Ile Th	_	Thr Ile	Asn Leu 270		Thr
Tyr Thr Leu 275	Glu Ala	Val Tyr	Glu Al 280	la Ile I	Phe Gly	Lys Pro 285	Lys	Glu
Lys Val Tyr 290	Ala Asp	Glu Ile 295	Ala Ly	ys Ala 1	Trp Glu 300	Ser Gly	Glu	Asn
Leu Glu Arg 305	Val Ala	Lys Tyr 310	Ser Me		Asp Ala 315	Lys Ala	Thr	Tyr 320

Glu Lei	ı Gly I	Lys Glu 325	Phe	Leu	Pro	Met	Glu 330	Ile	Gln	Leu	Ser	Arg 335	Leu
Val Gly		Pro Leu 340	Trp	Asp	Val	Ser 345	Arg	Ser	Ser	Thr	Gly 350	Asn	Leu
Val Glı	ı Trp P 355	Phe Leu	Leu	Arg	Lys 360	Ala	Tyr	Glu	Arg	Asn 365	Glu	Val	Ala
Pro Ası	_	Pro Ser		Glu 375	Glu	Tyr	Gln	Arg	Arg 380	Leu	Arg	Glu	Ser
Tyr The	Gly G	Gly Phe	Val 390	Lys	Glu	Pro	Glu	Lys 395	Gly	Leu	Trp	Glu	Asn 400
Ile Va	. Tyr I	Leu Asp 405	Phe	Arg	Ala	Leu	Tyr 410	Pro	Ser	Ile	Ile	Ile 415	Thr
His Ası		Ser Pro 120	Asp	Thr	Leu	Asn 425	Leu	Glu	Gly	Суз	Lys 430	Asn	Tyr
Asp Ile	e Ala P 435	Pro Gln	Val	Gly	His 440	Lys	Phe	Cys	Lys	Asp 445	Ile	Pro	Gly
Phe Ile		Ser Leu	Leu	Gly 455	His	Leu	Leu	Glu	Glu 460	Arg	Gln	Lys	Ile
Lys Th:	r Lys M	Met Lys	Glu 470	Thr	Gln	Asp	Pro	Ile 475	Glu	Lys	Ile	Leu	Leu 480
Asp Ty	Arg G	Gln Lys 485	Ala	Ile	Lys	Leu	Leu 490	Ala	Asn	Ser	Phe	Tyr 495	Gly
Tyr Ty	=	Tyr Ala 500	Lys	Ala	Arg	Trp 505	Tyr	Cys	Lys	Glu	Cys 510	Ala	Glu
Ser Vai	Thr A	Ala Trp	Gly	Arg	Lys 520	Tyr	Ile	Glu	Leu	Val 525	Trp	Lys	Glu
Leu Gli 530		Lys Phe	_	Phe 535	Lys	Val	Leu	Tyr	Ile 540	Asp	Thr	Asp	Gly

Leu Tyr 545	Ala Th	nr Ile	Pro 550	Gly	Gly	Glu	Ser	Glu 555	Glu	Ile	Lys	Lys	Lys 560
Ala Leu	Glu Ph	ne Val 565	Lys	Tyr	Ile	Asn	Ser 570	Lys	Leu	Pro	Gly	Leu 575	Leu
Glu Leu		yr Glu 30	Gly	Phe	Tyr	Lys 585	Arg	Gly	Phe	Phe	Val 590	Thr	Lys
Lys Arg	595				600			_		605		_	_
Leu Glu 610		-	-	615	-				620	-			
Ala Arg			630					635					640
Val Arg		645					650				_	655	
Pro Pro Glu Tyr	6 6	60				665				_	670		
Ala Lys	675				680					685	_		
690 Leu Arg				695					700		_		
705 Tyr Asp	_		710				_	715					720
Gln Val		725					730					735	
Lys Glu	74	40				745					750	_	
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<211> 776

<212> PRT

<213> Unknown

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<223> Variant derived from Pyrococcus furiosus Pfu-Polymerase

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Arg Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys 35 40 45

Ile Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val 50 60

Arg Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro 65 70 75 80

Ile Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr
85 90 95

Ile Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu
100 105 110

Tyr Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile 115 120 125

Pro Met Glu Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu 130 135 140

Ile Ser Ty	yr Ala Asp 165	Glu Asn	Glu Ala	Lys Val	Ile Thr	Trp Lys	Asn
Ile Asp Le	eu Pro Tyr 180	Val Glu	Val Val 185		Glu Arg	Glu Met 190	Ile
Lys Arg Pł	ne Leu Arg 95	Ile Ile	Arg Glu 200	Lys Asp	Pro Asp 205	Ile Ile	Val
Thr Tyr As	sn Gly Asp	Ser Phe	Asp Phe	Pro Tyr	Leu Ala 220	Lys Arg	Ala
Glu Lys Le 225	eu Gly Ile	Lys Leu 230	Thr Ile	Gly Arg 235	Asp Gly	Ser Glu	Pro 240
Lys Met G	ln Arg Ile 245	Gly Asp	Met Thr	Ala Val	Glu Val	Lys Gly 255	Arg
Ile His Ph	ne Asp Leu 260	Tyr His	Val Ile 265	-	Thr Ile	Asn Leu 270	Pro
Thr Tyr Th		Ala Val	Tyr Glu 280	Ala Ile	Phe Gly 285	Lys Pro	Lys
Glu Lys Va 290	al Tyr Ala	Asp Glu 295	Ile Ala	Lys Ala	Trp Glu 300	Ser Gly	Glu
Asn Leu Gi 305	lu Arg Val	Ala Lys 310	Tyr Ser	Met Glu 315	Asp Ala	Lys Ala	Thr 320
Tyr Glu Le	eu Gly Lys 325	Glu Phe	Leu Pro	Met Glu 330	Ile Gln	Leu Ser 335	Arg
Leu Val G	ly Gln Pro 340	Leu Trp	Asp Val	_	Ser Ser	Thr Gly 350	Asn
Leu Val G	lu Trp Phe 55	Leu Leu	Arg Lys	Ala Tyr	Glu Arg 365	Asn Glu	Val
Ala Pro As	sn Lys Pro	Ser Glu 375	Glu Glu	Tyr Gln	Arg Arg 380	Leu Arg	Glu

Ser Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu 385 390 395 400

Asn Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile 405 410 415

Thr His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn 420 425 430

Tyr Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro 435 440 445

Gly Phe Ile Pro Ser Leu Leu Gly His Leu L